

SEQUENCE LISTING

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HANAN, Eilat

<120> AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN
DIAGNOSING AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES

<130> SOLOMON=2C

<140> 09/830,954

<141> 2001-05-03

<150> PCT/IL00/00518

<151> 2000-08-31

<150> 09/629,971

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<150> US 09/473,653

<151> 1999-12-29

<150> US 60/152,417

<151> 1999-09-03

<160> 29

<170> PatentIn version 3.0

<210> 1

<211> 4

<212> PRT

<213> Artificial Sequence Sequence

<220>

<223> synthetic peptide

<400> 1

Glu Phe Arg His

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<210> 2

<211> 15

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<223> synthetic peptide

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 3

<211> 43

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<220>
<223> synthetic peptide

<400> 3

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
35 40

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<220>
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Trp Val Leu Asp
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(717)

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cag gtc aaa ctg cag gag tca ggg gct gag ctg gtg agg cct ggg gtc 48
Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val
1 5 10 15

tca gtg aag att tcc tgc aag ggt tct ggc tac aca ttc act gat tat 96
Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

gct atg cac tgg gtg aag cag agt cat gca aag agt cta gag tgg att 144
Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
35 40 45

gga gtt att agt act tac tat ggt gat gct agc tac aac cag aag ttc 192
Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe
50 55 60

aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc aca gcc tat 240
 Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

atg gaa ctt gcc aga ctg aca tct gag gat tct gcc atc tat tac tgt 288
 Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
 85 90 95

gca aga ggg gct act atg tcc tac ttt gac tac tgg ggc caa gtg acc 336
 Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr
 100 105 110

acg gtc acc gtc tcc tca ggt gga ggc ggt tca ggc gga gtt ggc tct 384
 Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Val Gly Ser
 115 120 125

ggc ggt ggc gga tcg gac atc gag ctc act cag tct cca gca atc atg 432
 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met
 130 135 140

tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca 480
 Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
 145 150 155 160

agt ata agt tac atg cac tgg tat cag cag aag cca ggc acc tcc ccc 528
 Ser Ile Ser Tyr Met His Trp Tyr Gln Lys Pro Gly Thr Ser Pro
 165 170 175

aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct 576
 Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
 180 185 190

cgc ttc agt ggc agt ggg tct ggg acc tct tat tct ctc aca atc agc 624
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
 195 200 205

agc atg gag gct gaa gat gct gcc act tat tac tgc cat cag cgg agt 672
 Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
 210 215 220

agt tac cca ttc acg ttc gga ggg ggg gcc aag ctg gaa ata aaa 717
 Ser Tyr Pro Phe Thr Phe Gly Gly Gly Ala Lys Leu Glu Ile Lys
 225 230 235

<210> 6
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 6

Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr
100 105 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Val Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met
130 135 140

Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
145 150 155 160

Ser Ile Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro
165 170 175

Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
195 200 205

Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
210 215 220

Ser Tyr Pro Phe Thr Phe Gly Gly Gly Ala Lys Leu Glu Ile Lys
225 230 235

<210> 7

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<212> PRT

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<220>
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Tyr Tyr Glu Phe Arg His
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<210> 8
<211> 15
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<220>
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<400> 8

Val His Glu Pro His Glu Phe Arg His Val Ala Leu Asn Pro Val
1 5 10 15

<210> 9
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 9

Lys Leu His
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<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<223> "n" at position 17 is unknown

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ccccctccg aacgtsnatg ggtaactcga tcgctgatgg cagta

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 11

atctatgcgg cccagccggc catg

24

<210> 12

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 12

gtggtgctga gtggatccta tactacactg ccaccggg

38

<210> 13

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 13

agctccgatg ctgaattcgg tgatagcggc tacgaagtgc atcatcagaa acctgcag

58

<210> 14

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

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ggtttctgat gatgcacttc gtagccgcta tcatgacgaa attcagcatc gg

52

<210> 15

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

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<400> 15

His Gln Arg Ser Ser Tyr Pro Cys Thr

1

5

<210> 16

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 16

His Gln Arg Ser Ser Tyr Pro Cys Thr
1 5

<210> 17

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 17

His Gln Arg Ser Ser Tyr Pro Phe Thr
1 5

<210> 18

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 18

His Gln Arg Ser Ser Tyr Pro Tyr Thr
1 5

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 19

His Gln Arg Ser Ser Tyr Pro Phe Thr
1 5

<210> 20

<211> 9

<212> PRT

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<220>

<223> synthetic peptide

<400> 20

His Gln Arg Ser Ser Tyr Pro Ser Thr
1 5

<210> 21
<211> 15
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<213> Artificial Sequence

<220>
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<400> 21

Asp Thr Glu Phe Arg His Ser Ser Asn Asn Phe Ser Ala Val Arg
1 5 10 15

<210> 22
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 22

Ser Thr Glu Phe Arg His Gln Thr Thr Pro Leu His Pro Asn Ser
1 5 10 15

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 23

Lys Glu Pro Arg His His Ile Gln His His Glu Arg Val Ile Arg
1 5 10 15

<210> 24
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 24

Ser Ala Ala Asp Phe Arg His Gly Ser Pro Pro Ile Ser Ala Phe
1 5 10 15

<210> 25
<211> 21

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 25

Lys Thr Asn Met Lys His Met Ala Gly Ala Ala Ala Ala Gly Ala Val
1 5 10 15

Val Gly Gly Leu Gly
20

<210> 26
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
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<400> 26

Asp Met Lys His
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<212> DNA
<213> Artificial Sequence

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<221> CDS
<222> (1)..(357)

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Gly Gly Ser Gly Gly Val Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu
1 5 10 15

ctc act cag tct cca gca atc atg tct gca tct cca ggg gag aag gtc 96
Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val
20 25 30

acc atg acc tgc agt gcc agc tca agt ata agt tac atg cac tgg tat 144
Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met His Trp Tyr
35 40 45

cag cag aag cca ggc acc tcc ccc aaa aga tgg att tat gac aca tcc 192
Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser
50 55 60

aaa ctg gct tct gga gtc cct gct cgc ttc agt ggc agt ggg tct ggg 240
 Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 65 70 75 80

acc tct tat tct ctc aca atc agc agc atg gag gct gaa gat gct gcc 288
 Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala
 85 90 95

act tat tac tgc cat cag cgg agt agt tac cca ttc acg ttc gga ggg 336
 Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Phe Thr Phe Gly Gly
 100 105 110

ggg gcc aag ctg gaa ata aaa 357
 Gly Ala Lys Leu Glu Ile Lys
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<210> 28
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 <212> PRT
 <213> Artificial Sequence

<400> 28

<220>
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Gly Gly Ser Gly Gly Val Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu
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Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val
 20 25 30

Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met His Trp Tyr
 35 40 45

Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser
 50 55 60

Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 65 70 75 80

Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala
 85 90 95

Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Phe Thr Phe Gly Gly
 100 105 110

Gly Ala Lys Leu Glu Ile Lys
 115

<210> 29
<211> 21
<212> PRT
<213> Mus sp.

<400> 29

Lys Thr Asn Leu Lys His Val Ala Gly Ala Ala Ala Ala Gly Ala Val
1 5 10 15

Val Gly Gly Leu Gly
20